

SK



PCT10

RAW SEQUENCE LISTING

DATE: 02/21/2003

PATENT APPLICATION: US/10/030,566A

TIME: 10:02:02

Input Set : N:\CrF4\01312003\J030566.raw

Output Set: N:\CRF4\02212003\J030566A.raw

1 <110> APPLICANT: Von Samson-Himmelstjerna, Georg
 2 Harder, Achim
 3 Schneider, Thomas
 4 Pape, Michaela
 5 <120> TITLE OF INVENTION: DNA Coding for Beta-Tubulin and Use Thereof
 6 <130> FILE REFERENCE: Mo6878/LeA 33 759
 7 <140> CURRENT APPLICATION NUMBER: US/10/030,566A
 8 <141> CURRENT FILING DATE: 2002-01-07
 9 <150> PRIOR APPLICATION NUMBER: PCT/EP00/06104
 10 <151> PRIOR FILING DATE: 2000-06-30
 11 <150> PRIOR APPLICATION NUMBER: DE19931883.2
 12 <151> PRIOR FILING DATE: 1999-07-09
 13 <160> NUMBER OF SEQ ID NOS: 2
 14 <170> SOFTWARE: PatentIn version 3.1
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 1380
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Cyathostomum coronatum
 20 <220> FEATURE:
 21 <221> NAME/KEY: CDS
 22 <222> LOCATION: (1)..(1344)
 23 <223> OTHER INFORMATION:

ENTERED

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 28 ggt tcc aag ttt tgg gaa gtg atc tct gac gag cat ggc att aag ccc 96
 29 Gly Ser Lys Phe Trp Glu Val Ile Ser Asp Glu His Gly Ile Lys Pro
 30 20 25 30
 31 gat ggc aca tac cac gga gaa tct gat cta caa tta gaa cga atc aat 144
 32 Asp Gly Thr Tyr His Gly Glu Ser Asp Leu Gln Leu Glu Arg Ile Asn
 33 35 40 45
 34 gtg tac tat aat gaa gca cat gga ggc aaa tat gtc cca cgt gca gtt 192
 35 Val Tyr Tyr Asn Glu Ala His Gly Gly Lys Tyr Val Pro Arg Ala Val
 36 50 55 60
 37 ctt gtt gat ctc gag ccc gga act atg gat tcc gtc cgt tcc ggg cca 240
 38 Leu Val Asp Leu Glu Pro Gly Thr Met Asp Ser Val Arg Ser Gly Pro
 39 65 70 75 80
 40 tac ggg caa ttg ttc cgc cct gat aac tac gtg ttt gga cag tct ggc 288
 41 Tyr Gly Gln Leu Phe Arg Pro Asp Asn Tyr Val Phe Gly Gln Ser Gly
 42 85 90 95
 43 gca gga aat aac tgg gca aaa ggt cac tac act gaa ggc gct gaa ctt 336
 44 Ala Gly Asn Asn Trp Ala Lys Gly His Tyr Thr Glu Gly Ala Glu Leu

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45		100		105		110		
46	gtc gac aat gta cta gat gta gtg cga aaa gaa gca gaa gga tgt gac							384
47	Val Asp Asn Val Leu Asp Val Val Arg Lys Glu Ala Glu Gly Cys Asp							
48		115		120		125		
49	tgt ctg cag ggc ttc cag cta act cac tca ctt gga gga ggt acc ggt							432
50	Cys Leu Gln Gly Phe Gln Leu Thr His Ser Leu Gly Gly Gly Thr Gly							
51		130		135		140		
52	tcg ggt atg ggc act ctc ctc atc tcc aaa att cgg gag gag tat cct							480
53	Ser Gly Met Gly Thr Leu Leu Ile Ser Lys Ile Arg Glu Glu Tyr Pro							
54		145		150		155		160
55	gat aga atc atg tcc tcg ttc tcc gtt gtc ccc tca cca aag gtc tcc							528
56	Asp Arg Ile Met Ser Ser Phe Ser Val Val Pro Ser Pro Lys Val Ser							
57		165		170		175		
58	gac act gtt gtg gag cct tac aat gct acc cta tcc gtt cat cag ttg							576
59	Asp Thr Val Val Glu Pro Tyr Asn Ala Thr Leu Ser Val His Gln Leu							
60		180		185		190		
61	gtt gaa aat aca gac gag act tat tgt att gac aat gaa gcc ctg tat							624
62	Val Glu Asn Thr Asp Glu Thr Tyr Cys Ile Asp Asn Glu Ala Leu Tyr							
63		195		200		205		
64	gat att tgc ttc cgc act ttg aaa ctc acg aac cca act tat gga gat							672
65	Asp Ile Cys Phe Arg Thr Leu Lys Leu Thr Asn Pro Thr Tyr Gly Asp							
66		210		215		220		
67	ctg aat cat ctt gtg tct gta aca atg tct ggt gtc acc aca tgt ctt							720
68	Leu Asn His Leu Val Ser Val Thr Met Ser Gly Val Thr Thr Cys Leu							
69		225		230		235		240
70	cgc ttc cct ggc caa ttg aat gcc gat cta cgc aaa cta gct gtt aac							768
71	Arg Phe Pro Gly Gln Leu Asn Ala Asp Leu Arg Lys Leu Ala Val Asn							
72		245		250		255		
73	atg gtt cca ttc cct cgt ctt cac ttc ttc atg cct ggt ttt gct cct							816
74	Met Val Pro Phe Pro Arg Leu His Phe Phe Met Pro Gly Phe Ala Pro							
75		260		265		270		
76	ctt tct gct aaa ggt gct cag gct tac cgt gct ctt acc gta gcc gag							864
77	Leu Ser Ala Lys Gly Ala Gln Ala Tyr Arg Ala Leu Thr Val Ala Glu							
78		275		280		285		
79	ctt aca cag cag atg ttt gat gct aag aat atg atg gct gct tgc gac							912
80	Leu Thr Gln Gln Met Phe Asp Ala Lys Asn Met Met Ala Ala Cys Asp							
81		290		295		300		
82	cct cga cat gga cgt tat ctc acc gtc gca gcc atg ttc cga gga aga							960
83	Pro Arg His Gly Arg Tyr Leu Thr Val Ala Ala Met Phe Arg Gly Arg							
84		305		310		315		320
85	atg agc atg agg gaa gta gac gac cag atg atg tca gtg cag aac aag							1008
86	Met Ser Met Arg Glu Val Asp Asp Gln Met Met Ser Val Gln Asn Lys							
87		325		330		335		
88	aac tcc tca tac ttc gta gag tgg atc ccg aac aac gtg aag acc gct							1056
89	Asn Ser Ser Tyr Phe Val Glu Trp Ile Pro Asn Asn Val Lys Thr Ala							
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91	gta tgc gac atc ccg cca cga gga ctg aag atg gcc gct acc ttc gtt							1104
92	Val Cys Asp Ile Pro Pro Arg Gly Leu Lys Met Ala Ala Thr Phe Val							
93		355		360		365		

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97      ttt aca gcc atg ttc cgc cgc aaa gcg ttc ttg cat tgg tac act ggt      1200
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99      385                               390                               395                               400
100     gaa ggt atg gac gag atg gag ttc act gaa gca gag tcc aac atg aat      1248
101     Glu Gly Met Asp Glu Met Glu Phe Thr Glu Ala Glu Ser Asn Met Asn
102     405                               410                               415
103     gat ctc atc tcc gag tac caa cag tac cag gaa gcc acc gct gac gac      1296
104     Asp Leu Ile Ser Glu Tyr Gln Gln Tyr Gln Glu Ala Thr Ala Asp Asp
105     420                               425                               430
106     atg ggc gat ctt gat gcg gaa ggc gct gaa gag gct tat cct gag gaa      1344
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112 <211> LENGTH: 448
113 <212> TYPE: PRT
114 <213> ORGANISM: Cyathostomum coronatum
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120     Asp Gly Thr Tyr His Gly Glu Ser Asp Leu Gln Leu Glu Arg Ile Asn
121     35      40      45
122     Val Tyr Tyr Asn Glu Ala His Gly Gly Lys Tyr Val Pro Arg Ala Val
123     50      55      60
124     Leu Val Asp Leu Glu Pro Gly Thr Met Asp Ser Val Arg Ser Gly Pro
125     65      70      75      80
126     Tyr Gly Gln Leu Phe Arg Pro Asp Asn Tyr Val Phe Gly Gln Ser Gly
127     85      90      95
128     Ala Gly Asn Asn Trp Ala Lys Gly His Tyr Thr Glu Gly Ala Glu Leu
129     100     105     110
130     Val Asp Asn Val Leu Asp Val Val Arg Lys Glu Ala Glu Gly Cys Asp
131     115     120     125
132     Cys Leu Gln Gly Phe Gln Leu Thr His Ser Leu Gly Gly Gly Thr Gly
133     130     135     140
134     Ser Gly Met Gly Thr Leu Leu Ile Ser Lys Ile Arg Glu Glu Tyr Pro
135     145     150     155     160
136     Asp Arg Ile Met Ser Ser Phe Ser Val Val Pro Ser Pro Lys Val Ser
137     165     170     175
138     Asp Thr Val Val Glu Pro Tyr Asn Ala Thr Leu Ser Val His Gln Leu
139     180     185     190
140     Val Glu Asn Thr Asp Glu Thr Tyr Cys Ile Asp Asn Glu Ala Leu Tyr
141     195     200     205
142     Asp Ile Cys Phe Arg Thr Leu Lys Leu Thr Asn Pro Thr Tyr Gly Asp
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144	Leu	Asn	His	Leu	Val	Ser	Val	Thr	Met	Ser	Gly	Val	Thr	Thr	Cys	Leu
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147				245						250					255	
148	Met	Val	Pro	Phe	Pro	Arg	Leu	His	Phe	Phe	Met	Pro	Gly	Phe	Ala	Pro
149				260					265					270		
150	Leu	Ser	Ala	Lys	Gly	Ala	Gln	Ala	Tyr	Arg	Ala	Leu	Thr	Val	Ala	Glu
151			275					280					285			
152	Leu	Thr	Gln	Gln	Met	Phe	Asp	Ala	Lys	Asn	Met	Met	Ala	Ala	Cys	Asp
153		290					295					300				
154	Pro	Arg	His	Gly	Arg	Tyr	Leu	Thr	Val	Ala	Ala	Met	Phe	Arg	Gly	Arg
155	305					310					315					320
156	Met	Ser	Met	Arg	Glu	Val	Asp	Asp	Gln	Met	Met	Ser	Val	Gln	Asn	Lys
157				325						330					335	
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159			340						345					350		
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161		355						360					365			
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163		370					375					380				
164	Phe	Thr	Ala	Met	Phe	Arg	Arg	Lys	Ala	Phe	Leu	His	Trp	Tyr	Thr	Gly
165	385					390					395					400
166	Glu	Gly	Met	Asp	Glu	Met	Glu	Phe	Thr	Glu	Ala	Glu	Ser	Asn	Met	Asn
167				405						410					415	
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VERIFICATION SUMMARY

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